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(54) Title: PCR AMPLIFICATION OF REARRANGED GENOMIC VARIABLE REGIONS OF IMMUNOGLOBULIN GENES

## (57) Abstract

The invention features methods for isolating immunoglobulin variable region genes, and the use of these genes in the production of chimeric and isotype switched antibodies. The invention also features substantially pure DNA encoding a variable region of the antibody produced by hybridoma cell line HNK-20, and chimeric antibodies containing this variable region.

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PCR AMPLIFICATION OF REARRANGED GENOMIC VARIABLE  
REGIONS OF IMMUNOGLOBULIN GENES

Background of the Invention

5       The development of mouse hybridoma technology has allowed the production of antibodies (Ab) specific for a wide range of antigens. Mouse monoclonal antibodies (mAb) have been used extensively for diagnosis and, in a few cases, for human therapy and *in vivo* diagnostics.

10      Administration of murine antibodies to humans has been observed to induce a strong human anti-mouse antibody response (HAMA) after single or repeated treatments, thus precluding long-term treatment using these antibodies.

15      Moreover, rodent antibodies are rapidly cleared from human serum and often do not interact effectively with the human immune system. Since human hybridomas are generally unstable and secrete low amounts of antibodies (frequently IgMs), considerable effort has been directed at rendering foreign antibodies (e.g., murine antibodies)

20      more similar to those of the host to which they are administered (e.g., a human). Alternatives to human hybridoma-derived antibodies have been developed in which mouse immunoglobulin sequences (e.g., constant regions) are replaced with corresponding sequences derived from

25      human immunoglobulin genes. Two examples of this type of antibody are (1) chimeric mAbs, in which murine variable regions are combined with human constant regions (Morrison et al., Proc. Natl. Acad. Sci. USA 81:6851-6855, 1984; Boulianne et al., Nature 312:643-646, 1984),

30      and (2) humanized mAbs, in which murine CDRs (complementarity determining regions) replace the corresponding sequences in human immunoglobulins (Jones et al., Nature 321:522-525, 1986; Co et al., Nature 351:501-502, 1991). These engineered antibodies retain

35      their target specificity and generally exhibit reduced

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HAMA responses when injected into patients. In addition, desired effector functions of antibodies for certain clinical applications can be obtained by using constant regions corresponding to the appropriate immunoglobulin 5 isotype.

Despite these advances, cloning of variable region sequences has been a limiting step in the rapid construction of chimeric and isotype switched antibodies. Polymerase chain reaction (PCR) amplification of 10 immunoglobulin heavy and light chain variable regions has facilitated this step. However, the high degree of DNA sequence polymorphism in leader and variable sequences of both heavy and light chain genes has required the preparation of complex sets of degenerate primers (Jones 15 et al., Bio/Technology 9:88-89, 1991; Kettleborough et al., Eur. J. Immunol. 23:206-211, 1993; Le Boeuf et al., Gene 82:371-377, 1989; Orlandi et al., Proc. Natl. Acad. Sci. USA 86:3833-3837, 1989). In the case of 5' primers, these primers have usually been designed to correspond to 20 the first framework of the variable region (FR1) and, in a few cases, to the leader peptide sequence (L). The 3' primers have usually been designed to correspond to the framework 4 (FR4) region, which displays limited polymorphism, or to the constant region, in which 25 conserved, isotype-specific sequences are easily identified. Although complex sets of 5' and 3' primers have been designed, they do not always match the DNA template completely (Gavilondo-Cowley et al., Hybridoma 9:407-417, 1990; Leung et al., BioTechniques 15:286-292, 30 1993). Native sequences of the immunoglobulin heavy and light chain genes may therefore be altered in the FR1 and/or FR4 regions by the PCR amplification process. Modifications of the N-terminal region of an 35 immunoglobulin, particularly the light chain variable region (VL), in which the amino acid at position two is

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part of the predicted canonical structure for CDR1 (Chothia et al., Nature 342:877-883, 1989), have been shown to drastically reduce the affinity of immunoglobulins for their antigens. Moreover, expression 5 levels of the recombinant antibodies may also be altered when mutations occur in the leader peptide. In most studies involving PCR amplification of immunoglobulin H (heavy) and  $\kappa/\lambda$  (light) chain variable regions using these primers, cDNA templates were used, resulting in the 10 generation of fragments containing incomplete VH and VL sequences, which may or may not be linked to part of the constant region.

#### Summary of the Invention

We have designed a method for isolating nucleic acids encoding immunoglobulin Fv (variable) fragments from genomic DNA of hybridoma cells producing specific monoclonal antibodies. Specific primers corresponding to 15 (1) the 5' untranslated region (UTR) of the variable region and (2) the intron downstream of the rearranged 20 JH/J $\kappa/\lambda$  sequences are used in this method. The method can be used to amplify and clone genomic DNA corresponding to  $\lambda$  and  $\kappa$  light chain variable genes, as well as heavy chain variable genes. The variable genes isolated by this method can easily be inserted into 25 expression vectors containing heterologous (e.g., human) light and heavy chain constant genes, thus facilitating isotype switching or antibody chimerization. Using this method, we have cloned for the first time genes encoding the variable regions (Fv) of the kappa light chain and 30 heavy chain of the antibody produced by hybridoma cell line HNK-20.

Accordingly, in one aspect the invention features substantially pure DNA (genomic DNA or cDNA) encoding a variable region of the antibody produced by hybridoma

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cell line HNK-20. The variable region can be from the immunoglobulin heavy chain of the antibody, or from the immunoglobulin light chain of the antibody. The DNA may further encode an immunoglobulin constant region, such as 5 a human immunoglobulin constant region. The immunoglobulin can be of any isotype, including, but not limited to an IgA (e.g., IgA1, IgA2, and sIgA), IgG, IgM, IgD, or IgE isotype. In the case of an IgA isotype, the immunoglobulin heavy chain can be an  $\alpha$  chain.

10 In one embodiment, the substantially pure DNA contains the sequence of Fig. 5B, or degenerate variants thereof, and encodes the amino acid sequence of Fig. 5B. In another embodiment, the substantially pure DNA contains a sequence having about 50% or greater sequence 15 identity to the DNA sequence of Fig. 5B. In another embodiment, the substantially pure DNA a) is capable of hybridizing to the DNA sequence of Fig. 5B under stringent conditions; and b) encodes a polypeptide having a biological activity of a HNK-20 variable region.

20 In another embodiment, the substantially pure DNA contains the sequence of Fig. 5C, or degenerate variants thereof, and encodes the amino acid sequence of Fig. 5C. In another embodiment, the substantially pure DNA contains a sequence having about 50% or greater sequence 25 identity to the DNA sequence of Fig. 5C. In another embodiment, the substantially pure DNA a) is capable of hybridizing to the DNA sequence of Fig. 5C under stringent conditions; and b) encodes a polypeptide having a biological activity of a HNK-20 variable region.

30 In another embodiment, the substantially pure DNA contains the sequence of Fig. 5D, or degenerate variants thereof, and encodes the amino acid sequence of Fig. 5D. In another embodiment, the substantially pure DNA contains a sequence having about 50% or greater sequence 35 identity to the DNA sequence of Fig. 5D. In another

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embodiment, the substantially pure DNA a) is capable of hybridizing to the DNA sequence of Fig. 5D under stringent conditions; and b) encodes a polypeptide having a biological activity of a HNK-20 variable region.

5 In another aspect of the invention, the DNA is operably linked to regulatory sequences, such as promoter and/or enhancer sequences, for expression of the variable region. In a related aspect, the invention features a vector (e.g., a plasmid or a viral vector) containing the  
10 DNA of the invention operably linked to a promoter sequence. The invention also features a cell (e.g., a myeloma cell) containing the DNA of the invention.

In another aspect, the invention features a recombinant antibody containing a variable region from  
15 the monoclonal antibody produced by hybridoma cell line HNK-20. In one embodiment, the variable region is from the immunoglobulin heavy chain of the monoclonal antibody. In another embodiment, the variable region is from the immunoglobulin light chain of the monoclonal  
20 antibody. The recombinant antibody may further contain a chimeric constant region, e.g., a human immunoglobulin constant region. The antibody of the invention may be of any immunoglobulin isotype, such as those listed above. Accordingly, the antibody of the invention may contain an  
25 a heavy chain, and thus be of the IgA isotype.

The invention also features a method of making a recombinant antibody containing a variable region from the monoclonal antibody produced by hybridoma cell line HNK-20. This method involves expression of DNA encoding  
30 the variable region of the antibody, as well as a constant region (e.g., a human constant region). Expression of the DNA may be carried out using any standard method known in the art. Preferably, the DNA is expressed in a cell, e.g., a myeloma cell. The cell is  
35 cultured under conditions in which the recombinant

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antibody is produced, and the antibody is subsequently purified from the cell or from the supernatant in which the cell was cultured, using standard methods.

In a final aspect, the invention features a method 5 of isolating a nucleic acid containing a variable region of an immunoglobulin gene (e.g., the immunoglobulin gene is from hybridoma cell line HNK-20). In this method, a first set of primers, each of which contains the sequence of a polymorphic variant of a segment of the 5' 10 untranslated region of said immunoglobulin gene; and a second set of primers, each of which contains the sequence of a polymorphic variant of a segment of the intron 3' to the rearranged J region of said immunoglobulin gene; are used in a polymerase chain 15 reaction containing genomic DNA that encodes the variable region of the immunoglobulin. A set of primers that contain sequences of the immunoglobulin gene is identified from the polymerase chain reaction, and subsequently is used to amplify the immunoglobulin gene.

20 By "promoter" is meant a minimal sequence element sufficient to direct transcription. Also included in the invention are those promoter elements which are sufficient to render promoter-dependent gene expression controllable for cell-type or tissue-specific expression, 25 as well as elements which allow expression to be inducible by external signals or agents; such elements may be located in the 5' or 3' regions of, as well as within, the native gene.

By "operably linked" is meant that a gene and a 30 regulatory sequence(s) are connected in such a way as to permit gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequence(s).

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By "substantially identical" is meant a polypeptide or nucleic acid exhibiting at least 50%, preferably 85%, more preferably 90%, and most preferably 95% homology to a reference amino acid or nucleic acid sequence. For polypeptides, the length of comparison sequences will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 30 nucleotides, preferably at least 50 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides.

Sequence identity is typically measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705; Ausubel et al., eds. Current Protocols in Molecular Biology, Wiley & Sons, New York, 1989). Such software matches similar sequences by assigning degrees of homology to various substitutions, deletions, substitutions, and other modifications. Conservative substitutions for amino acids typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

By "substantially pure DNA" is meant DNA that is free of the genes which, in the naturally-occurring genome of the organism from which the DNA is derived, flank the gene. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g.,

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a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

"Stringent conditions", as used herein, are defined as follows. High stringency conditions include hybridization at about 42°C in about 50% formamide; a first wash at about 65°C in about 2x SSC and 1% SDS; followed by a second wash at about 65°C in about 0.1% SSC. Lower stringency conditions for genes having about 50% sequence identity include hybridization at about 42°C in the absence of formamide; a first wash at about 42°C in about 6x SSC and about 1% SDS; followed by a second wash at about 50°C in about 6x SSC and about 1% SDS.

Our method for isolating immunoglobulin variable region genes, using genomic DNA templates, does not lead to the production of fragments that need to be adapted for recombinant antibody expression, thus facilitating the generation of chimeric and isotype-switched immunoglobulins. Variable regions with intact coding sequences, including full length leader peptides, are obtained using this method without requiring previous DNA sequencing. Thus, isotype switched mouse Ig and chimeric mouse-human Ig can easily be produced. Chimeric antibodies containing constant regions derived from the host to which the antibody is to be administered (e.g., a human), are advantageous for use in therapeutics, because such chimeric antibodies are less likely than heterologous antibodies (e.g., murine antibodies) to lead to an adverse immune response, e.g., an HAMA response, in the patient.

Other features and advantages of the invention will be apparent from the following detailed description and from the claims.

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Detailed Description

The drawings are first described.

Drawings

Figs. 1A-1B are schematic representations of  
5 rearranged genes encoding the variable regions of heavy  
(Fig. 1A), kappa (Fig. 1B), and lambda (Fig. 1C) mouse  
immunoglobulin chains. Pseudogenes are indicated  
by "p"s. Bold arrows indicate PCR primers corresponding  
to the 5' untranslated region and the intron downstream  
10 of the rearranged J segment. SalI and NotI restriction  
sites have been added to the 5' ends of the PCR primers.  
Arrows below the J segments represent oligonucleotide  
probes used in Northern and Southern blot hybridization.

Figs. 2A and 2B are Northern blots of RNA isolated  
15 from hybridoma cell lines 3G3 and HNK-20 probed with  
oligonucleotides homologous to the JH, J $\kappa$ , and J $\lambda$   
segments. Fig. 2A: Total RNA (10  $\mu$ g per slot) from  
hybridoma cell line 3G3 (IgM,  $\lambda$ ) was hybridized with  
oligonucleotides J $\lambda$ 1, J $\lambda$ 2, and J $\lambda$ 3, as indicated in the  
20 figure. Fig. 2B: Total RNA (10  $\mu$ g per slot) from HNK-20  
(IgA,  $\kappa$ ) was hybridized with J $\kappa$ 1, J $\kappa$ 2, J $\kappa$ 4, and J $\kappa$ 5; and  
JH1, JH2, JH3, and JH4 (see Fig. 6 for the sequence of  
the oligonucleotide probes), as indicated.

Oligonucleotides specific for the pseudogenes (J $\kappa$ 3 and  
25 J $\lambda$ 4) were not used in these experiments. As an internal  
control for total RNA loading, the blots were  
rehybridized with a full length glyceraldehyde-3-  
phosphate-dehydrogenase (GAPDH) cDNA probe (McMaster et  
al., Proc. Natl. Acad. Sci. USA 74:4835-4838, 1977).  
30 Migration positions of ribosomal RNA are indicated.

Figs. 3A-3G are Southern blots of amplified 3G3  
V $\lambda$ , HNK-20 V $\kappa$ , and HNK-20 VH genomic fragments, made by  
following a two step PCR amplification method. In the  
first step (Figs. 3A-3D), PCR amplification was carried  
35 out using groups of 2, 3, or 4, 5' primers (see Fig. 6)

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and a single 3' primer. The 3' primer for V $\lambda$  was: 3' $\lambda$ 1, for V $\kappa$ : 3' $\kappa$ 2, and for VH: 3'H3a or 3'H3b. In the second step (Figs. 3E-3G), PCR amplification was performed separately with each of the 5' primers from the positive 5 groups from the first set of reactions (Figs. 3A-3D), allowing identification of the 5' primer(s) that generate(s) the signal in each positive group. PCR amplification with 3'H3a was omitted in the second step since 3'H3b generates stronger signals. Positions of 10 size markers of 564, 831, and 947 basepairs are indicated in the lane labelled M1.

Figs. 4A-4B are schematic representations of the rearranged 3G3 V $\lambda$ , HNK-20 V $\kappa$ , and VH regions. In Fig. 4A rearrangement of the lambda locus from 3G3 is shown. In 15 Fig. 4B rearrangements of the kappa and heavy chain loci from HNK-20 are shown. Three different kappa chain gene rearrangements have been observed with the J $\kappa$ 2 segment. For the heavy chain genes, 5'H31a and 5'H31b generate the same PCR product, hence a single rearrangement is 20 observed for the heavy chain. The maps are not drawn to scale.

Figs. 5A-5D are sequences of the PCR amplified 3G3 V $\lambda$ , HNK-20 V $\kappa$ , and HNK-20 VH regions. The sequences shown in Figs. 5A, 5B, 5C, and 5D correspond to 3G3 V $\lambda$  25 (generated by 5' $\lambda$ 1-3' $\lambda$ 1), HNK-20 V $\kappa$  (generated by 5' $\kappa$ 16-3' $\kappa$ 2), HNK-20 V $\kappa$  (generated by 5' $\kappa$ 30-3' $\kappa$ 2), and HNK-20 VH (generated by 5'H31b-3'H3b), respectively. The sequences of the PCR primers are shown in bold, the CDR regions are underlined, and stop codons are indicated by stars. 30 Regions homologous to the J $\lambda$ , J $\kappa$ , and JH oligonucleotide probes are double underlined.

Figs. 6A-6F are the nucleotide sequences of the PCR primers and probes used for the amplification of mouse V $\lambda$ , V $\kappa$ , and VH regions. SalI and NotI sites are in 35 bold, and I represents inosine. Sequences are 5' to 3'.

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The names of the groups of 5' primers precede the numbering and sequences of the primers.

The Monoclonal Antibody Produced by Hybridoma Cell Line HNK-20.

5        Respiratory Syncytial Virus (RSV) infection can lead to diseases of the upper or lower respiratory tract, including pneumonia and severe bronchiolitis (McIntosh et al., In B. N. Fields and D. M. Knipe (eds.), Virology, Raven Press, New York, pp. 1045-1072, 1990). HNK-20 is a  
10 murine hybridoma cell line that produces a monoclonal IgA antibody that recognizes the F glycoprotein of RSV. In addition to neutralizing RSV in plaque reduction assays, this antibody is effective at preventing and treating RSV infection when passively administered to mice  
15 intranasally.

Method for Isolating Immunoglobulin Variable Region Genes.

We have designed a strategy for the preparation of genomic fragments encoding the VH-D-JH (immunoglobulin heavy chain variable region) and VL-JL (immunoglobulin light chain variable region) regions of immunoglobulin genes. This strategy involves PCR amplification of genomic DNA prepared from hybridomas using specific primers corresponding to (1) the 5' untranslated region  
20 of the gene encoding the variable region, and (2) an intron downstream from specific rearranged JH/JL  
25 sequences. This method does not require previous knowledge of the sequence of any part of the gene encoding the target variable region, thus allowing rapid  
30 and efficient isolation of the genes.

Based on analysis of nucleotide sequence databases (e.g., the Genbank), sets of primers are designed corresponding to all of the sequences reported in the

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databases for a given organism (e.g., a mouse) for a specific region within the 5' UTR of the immunoglobulin variable region gene and for a specific region in the intron downstream of the rearranged J segment. In order 5 to minimize the numbers of primers required to cover all of the possible known sequences for a given region (e.g., the 5' UTR), the most highly conserved specific regions within the region may be focused on. As a specific example, in the case of the 5' UTR of the murine variable 10 heavy chain, 42 primers are required because of the relatively high degree of nucleotide sequence polymorphism (see below). In contrast, due to lower levels of sequence polymorphism, only 2 primers are required to cover all of the known possibilities for the 15 5' UTR of the murine immunoglobulin lambda variable region (see below). In a first set of PCR reactions, multiple primers covering all of the polymorphic sequences corresponding to the region the primers hybridize to can be used in a single reaction. In cases 20 where a large number of primers are required, the primers can be divided up into several reactions based on, e.g., their melting temperatures. For example, for the 5' UTR of the murine heavy chain variable region, where 42 primers are required to cover all of the known 25 polymorphic sequences, the reactions were divided up into 12 groups (see below). Primers contained in those reactions of the first set of PCR reactions found to be positive can subsequently be tested individually (i.e., in reactions containing only a single 5' primer and a 30 single 3' primer) in order to identify the sets of primers that correspond to the sequence of the gene being amplified. These primers can then be used to prepare the fragment for cloning, in order to generate chimeric or isotype switched immunoglobulin genes. As no sequence 35 information for the gene being amplified is required in

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the present method, isolating variable region genes from hybridoma cell lines is facilitated.

Variable regions isolated by this method can be fused to genes encoding heterologous constant regions in order to produce chimeric (e.g., a murine variable region fused to a human constant region) or isotype switched immunoglobulin genes, that can in turn be used to make chimeric or isotype switched antibodies. We have used this method to produce chimeric immunoglobulin genes, including one containing the HNK-20 heavy chain variable region fused to a human heavy chain constant region, and another containing the HNK-20 kappa light chain variable region fused to a human kappa light chain constant region. Co-expression of these genes leads to the production of recombinant antibodies having the specificity of the antibody produced by hybridoma cell line HNK-20, and the effector regions of a human antibody.

The recombinant antibodies of the invention can be used to prevent RSV infection, or to treat diseases caused by RSV infection (e.g., upper or lower respiratory tract infections, such as pneumonia or bronchiolitis). The recombinant antibodies of the invention may be administered to any hosts that are susceptible to RSV infection, including, but not limited to, humans (adults, children, and infants), chimpanzees, cattle, cebus monkeys, owl monkeys, ferrets, lambs, mice, rats, and cotton rats. The therapeutic compositions of the invention may be administered to a patient by any appropriate mode. Typically, the antibody is administered to a mucosal surface of the subject, for example, an oral or an intranasal surface. The antibodies of the invention can be administered in an amount determined to be effective for prevention or treatment of RSV infection by one skilled in the art. An

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appropriate dosage is one which effects a reduction in the disease caused by RSV infection, and/or one which is effective at preventing RSV infection. It is expected that the dosages will vary, depending upon the mode and 5 route of administration; the age, weight, and health of the recipient; the nature and extent of the disease; the frequency and duration of the treatment; the type, if any, concurrent therapy; and the desired effect. For example, the amount of antibody administered may be in 10 the range of 50 µg/kg to 5 mg/kg body weight. The invention also includes compositions containing the antibodies of the invention in a pharmaceutically acceptable carrier and/or diluent, e.g., saline. Suitable pharmaceutical carriers, as well as 15 pharmaceutical necessities for use in pharmaceutical formulations, are described in *Remington's Pharmaceutical Sciences*, a standard reference text in this field, and in the USP/NF.

The antibodies of the invention may also be used 20 in diagnostic methods for identifying patients infected with RSV, using any of a number of standard assay systems that are well known in the art. Such assay systems include, but are not limited to, enzyme linked immunosorbent assays (ELISA), solid phase radiometric 25 assays, immunofluorescent microscopy, and immunolectron microscopy (see, e.g., Coligan et al., eds., Current Protocols in Immunology, John Wiley & Sons, New York, 1992). In these methods, an antigen (e.g., from a biological sample, such as cellular material or 30 secretions) is contacted with an antibody of the invention, and specific binding of the antigen and the antibody is detected as a measure of the presence of the antigen in the sample. The detection can be facilitated by the presence of labels on the antibodies of the 35 invention or labels on secondary antibodies that

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recognize the antibodies of the invention. The labels that can be employed in these assays include, but are not limited to, radio-labels, enzyme labels (e.g., horse-radish peroxidase), biotin-labels, and chemiluminescent labels, and are detected using standard methods.

5 Genes encoding immunoglobulin variable regions (both light (kappa and lambda) and heavy chains) isolated using the methods of the present invention can be fused to genes encoding immunoglobulin constant regions (e.g., 10 human constant region genes) in order to make genes encoding chimeric or isotype switched recombinant antibodies (see, e.g., United States Patent Number 4,816,397, issued March 28, 1989; hereby incorporated by reference; and Morrison et al., Proc. Natl. Acad. Sci. 15 USA 81:6851-6855, 1984; hereby incorporated by reference). For example, in order to generate an IgA antibody, the variable region can be fused to an  $\alpha$  constant region. Different types of constant regions that can be used to make the chimeric antibodies of the 20 invention are well known in the art (see, e.g., Roitt et al., eds. Immunology, Gower Medical Publishing, London, 1989), and can be isolated and cloned to make the chimeric and/or isotype switched genes of the invention using standard methods (see, e.g., Sambrook et al., eds. 25 Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989; and Coligan et al., *supra*). In order to facilitate cloning of the variable genes into vectors, preferably, the PCR primers used in their amplification contain in 30 their 5' ends sequences recognized by restriction endonucleases. Vectors into which the variable region genes and chimeric genes of the invention can be cloned include both plasmid and viral vectors. Preferred vectors for use in the invention are expression vectors 35 containing appropriate heterologous heavy or light chain

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constant genes. For example, genes encoding kappa light chain and heavy chain variable regions can be cloned into plasmids such as pUHW $\kappa$  and pUHW $\gamma$ 1, respectively (Weissenhorn et al., Gene 106:273-277, 1991, hereby 5 incorporated by reference). These plasmids contain a combination of a heavy-chain enhancer and a  $\mu$ -gene promoter, as well as a polylinker into which genes encoding variable regions can be inserted. Another vector that can be used in the invention is the pING 10 expression vector (Chomczynski et al., Biochem. Biophys. Res. Commun. 122:340-344, 1984, see below).

The genes of the invention are cloned into the vectors so that the genes are operably linked to appropriate promoter/enhancer sequences. Any promoter 15 that is capable of directing initiation of transcription in a eukaryotic cell may be used in the invention. For example, non-tissue specific promoters, such as the cytomegalovirus (DeBernardi et al., Proc. Natl. Acad. Sci. USA 88:9257-9261, 1991, and references therein), 20 mouse metallothioneine I gene (Hammer et al., J. Mol. Appl. Gen. 1:273-288, 1982), HSV thymidine kinase (McKnight, Cell 31:355-365, 1982), and SV40 early (Benoist et al., Nature 290:304-310, 1981) promoters may be used. Preferred promoters for use in the invention 25 include those which direct expression in myeloma cells, as are described above.

Expression of the genes encoding the chimeric and/or isotype switched antibodies of the invention can be achieved using any of a number of methods standard in 30 the art. For example, vectors, e.g., plasmids, containing the HNK-20 variable region(s) fused to heterologous constant regions can be transfected into a cell in which the gene is expressed, either constitutively or upon induction. The genes can be 35 transfected into the cells using any standard method in

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the art, including, but not limited to, electroporation, calcium phosphate precipitation, protoplast fusion, and the use of viral vectors or lipids that are coupled with the genes (see, e.g., Sambrook et al., *supra*). Any cell 5 in which the genes of the invention can be expressed to produce the antibodies of the invention may be used. Such cells include, but are not limited to, myeloma cells, such as non-Ig-producing myeloma cells. As a specific example, Sp2/0-Ag14 cells, which are murine 10 myeloma cells that do not secrete or synthesize any immunoglobulin chains, can be used. Sp2/0-Ag14 cells can be obtained from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852-1776, and have been designated ATCC CRL 1581 (see also Ochi et al., 15 Proc. Natl. Acad. Sci. USA 80:6351-6355, 1983). Other cell lines that can be used in the invention include P3X63Ag8.653 (ATCC CRL 1580) and Sp2/01-Ag (ATCC CRL 8006).

The antibodies of the invention can be produced by 20 culturing cells expressing the genes encoding them using standard methods. The antibodies are then purified from the cells and/or cell culture supernatants using standard methods (see, e.g., Coligan et al., *supra*). The culture conditions may be scaled-up using standard methods, in 25 order to generate large quantities of antibody. In addition, the antibodies may be purified from ascites using standard methods.

#### Experimental Results

Design of the primers and probes for PCR amplification of 30 mouse VH and VL genes.

Most strategies used to amplify mouse VH and VL genes generate fragments encoding variable regions that are either truncated or contain mutations in their 5' and/or 3' ends. We have developed a PCR method for

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amplifying Fv (variable) genes that results in preservation of the entire Fv sequence. The primers used in this method hybridize to the 5' untranslated region (the 5' primers) and in the intron downstream of the 5 rearranged J segment of the lambda, kappa, and heavy chain genes (the 3' primers; Fig. 1).

DNA sequence comparisons of 5' untranslated regions and introns downstream from J segments were performed using data from Kabat (Kabat et al., Sequences 10 of Proteins of Immunological Interest, 5th Ed., U.S. Dept. Health and Human Services, Washington, DC, 1991) and the Genbank and European Molecular Biology Laboratory (EMBL) libraries, and were further analyzed with the Genetics Computer Group (GCG, Madison, WI) package 15 programs. Alignment of the DNA sequences of the 5' untranslated region revealed that the polymorphism in this region is globally identical to that of the leader peptide sequences. However, a stretch of around 20 nucleotides immediately upstream of the start codon (ATG) 20 was observed to be more conserved throughout the alignment. We therefore designed a series of 5' PCR primers (18-mers) that terminate with the ATG sequence, ensuring perfect matches of the 3' ends of each primer with the template, as is critical for initiation of 25 consistent priming by Taq polymerase. A SalI restriction site and 4 additional nucleotides, which facilitate digestion by the restriction endonuclease, were added to the 5' end of the primers in order to expedite cloning of the PCR fragments. Complex sets of 5' primers were 30 synthesized consisting of 2 primers for lambda, 30 primers for kappa, and 42 primers for the heavy chain genes, some of which primers contained inosine residues, or were degenerate (Fig. 6).

In contrast, alignment of the 5' end of the intron 35 sequences downstream from the J segments did not reveal

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significant polymorphism, so that 3' PCR primers specific for each of the J $\lambda$ , J $\kappa$ , and JH segments were designed in this intronic region. Single PCR primers were prepared corresponding to the regions downstream from each J  
5 segment, except for the JH3 segment, for which 2 primers were needed because of DNA sequence polymorphism. The 3' PCR primers are 18-mers, except for the primer downstream of the JH1 segment which was designed as a 20-mer because of the high A/T content of this region. A NotI  
10 restriction site and 4 additional nucleotides were added to the 5' end of these oligonucleotides in order to allow directional cloning of the PCR fragments into expression vectors (Fig. 6).

In order to ensure specificity of the PCR  
15 amplifications and to better characterize the VH-D-JH and VL-JL rearrangements, JL and JH-specific oligonucleotide probes were designed. Sets of oligonucleotides (19-mers) specific for each of the J $\lambda$ , J $\kappa$ , and JH segments, which exhibit very low polymorphism, were synthesized. These  
20 oligonucleotides were used as probes in both Southern blot analysis of the PCR fragments, and Northern blot analysis of total RNA extracted from mouse hybridoma cells.

**Specificity of the oligonucleotide probes.**  
25 The specificity of the oligonucleotide probes homologous to each J segment in DNA-DNA hybridization was demonstrated by Southern blot hybridization using a variety of cloned VL and VH PCR fragments of known sequences. The specificity of these probes was also  
30 tested by hybridization to RNA on Northern blots. RNA from the hybridoma cells 3G3 (IgM,  $\lambda$ ) and HNK-20 (IgA,  $\kappa$ ) were hybridized with the J $\lambda$ , J $\kappa$ , and JH oligonucleotides (Fig. 2). The Northern blot analysis revealed that probes J $\lambda$ 1, J $\kappa$ 2, and JH3 generate signals at the expected  
35 sizes for 3G3 and HNK-20, respectively. Hybridization of

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HNK-20 RNA with the J $\kappa$ 2 probe generated a much stronger signal than the JH3 probe, although these two probes had similar specific activities and identical calculated melting temperatures. This observation suggests either 5 that the kappa chain transcript is much more abundant, or that several kappa chain transcripts hybridize with the J $\kappa$ 2 probe. PCR amplification of the V $\kappa$  region supports the hypothesis that there are several different kappa chain gene rearrangements, one of which was derived from 10 a transcribed pseudogene rearranged with the J $\kappa$ 2 segment present in the immortalized fusion partner X63Ag8.653 (Strohal et al., Nucleic Acids Res. 15:2771, 1987; Carroll et al., Mol. Immunol. 25:991-995, 1988). Thus, at least one kappa pseudogene and one kappa functional 15 gene transcript, both rearranged with the J $\kappa$ 2 segment, are contributing to the strong signal observed. The Northern blots were then rehybridized with a probe specific for the house-keeping enzyme gene glyceraldehyde-3-phosphate-dehydrogenase (Piechaczyk et 20 al., Nucleic Acids Res. 12:6951-6963, 1984) to control for the amount of RNA loaded (Fig. 2).

Use of the above-described J-specific oligonucleotide probes allows rapid characterization of the PCR products and immunoglobulin gene transcripts, and 25 further allows identification of the J segment used in the rearrangement of the light and heavy chain genes.

#### Amplification and detection of mAb variable region genes.

Several immunoglobulin variable region genes have been amplified by PCR using genomic DNA prepared from 30 mouse hybridoma cells. As specific examples, amplification of the V $\lambda$  gene of the hybridoma cell line 3G3, and the V $\kappa$  gene and VH genes of hybridoma cell line HNK-20 are described.

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Based on the Northern blot analysis shown in Fig. 2, it was established that the  $\lambda$  chain gene was rearranged with  $J\lambda 1$ , the  $\kappa$  chain gene was rearranged with  $J\kappa 2$ , and the heavy chain gene was rearranged with  $JH3$ . Therefore, the 3' primers required for amplification were  $3'\lambda 1$ ,  $3'\kappa 2$ , and  $3'H3a/3'H3b$ . Due to the high level of polymorphism in the 5' untranslated region, if all of the 5' primers were used in separate PCR reactions, there would be 2 PCR reactions for lambda, 30 PCR reactions for kappa, and 42 PCR reactions for the heavy chain genes. To reduce this complexity, the 5' primers were divided into small groups of 2, 3, or 4 primers based on their melting temperatures (Fig. 6). One group was required for  $\lambda$ , 9 for  $\kappa$ , and 12 for the heavy chain gene primers, reducing the number of reactions to 1, 9, and 12, respectively.

The fragments produced in the first set of PCR amplification reactions, as analyzed on Southern blots hybridized with the  $J\lambda 1$ ,  $J\kappa 2$ , and  $JH3$  probes, corresponded to the expected sizes in the 5' $\lambda$  group a, in the 5' $\kappa$  groups g and i, and in the 5' $H$  groups c and l (Figs. 3A, 3B, 3C, and 3D). In the second set of PCR reactions, each 5' primer from the positive groups identified in the first set of PCR reactions was combined with the corresponding 3' primer, and the amplified fragments were analyzed on Southern blots using the  $J\lambda 1$ ,  $J\kappa 2$ , and  $JH3$  oligonucleotide probes. This experiment revealed that 5' $\lambda 1$ , 5' $\kappa 30$ , 5' $\kappa 16$ , 5' $\kappa 19$  and 5' $H31B$  generate the predicted signals (Figs. 3E, 3F, and 3G), indicating that rearranged fragments were found for one lambda chain gene in 3G3, 3 kappa chain genes in HNK-20, and one heavy chain gene in HNK-20 (Fig. 4). Using another mouse hybridoma cell (PCG-4), secreting IgG2a with a  $\kappa$  chain, 3 different rearrangements of the kappa chain genes, and a single rearrangement of the heavy

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chain gene, were observed using the same PCR strategy. This observation is consistent with the presence of both a functional  $\text{V}\kappa$  and aberrant  $\text{V}\kappa$  transcripts in hybridoma cells obtained by fusion using cell lines derived from 5 the original MOPC-21 tumor (Strohal et al., Nucleic Acids Res. 15:2771, 1987; Carroll et al., Mol. Immunol. 25:991-995, 1988). A third non-transcribed kappa chain rearrangement was detected in both HNK-20 and PCG-4 hybridomas which involved different  $\text{J}\kappa$  segments. Since 10 the only  $\kappa$ -chain gene that the fusion partner can contribute is the non-functional MOPC-21  $\kappa$  gene (Storb et al., Nucleic Acids Res. 8:4681-4687, 1980), this third rearrangement probably originated from the mouse B-cell that served as a fusion partner.

15 **Sequence analysis of the  $\text{V}\lambda$ ,  $\text{V}\kappa$ , and  $\text{VH}$  PCR fragments.**  
The PCR amplified variable regions of 3G3  $\text{V}\lambda$ , HNK-20  $\text{V}\kappa$ , the HNK-20  $\text{V}\kappa$  pseudogene, and HNK-20  $\text{VH}$  were each cloned into the pING expression vector (Chomczynski et al., *supra*) and sequenced using the dideoxy chain 20 termination method (Piechaczyk et al., Nucleic Acids Res. 12:6951-6963, 1984). The corresponding sequences are shown in Figs. 5A-5D. The deduced amino acid sequences of the  $\text{V}\lambda$ ,  $\text{V}\kappa$ , and  $\text{VH}$  fragments correspond to open reading frames consistent with those reported in the 25 various gene banks. In all three PCR amplified fragments, the positions of the cysteines involved in intramolecular disulfide bridge formation were conserved. The presence of conserved stretches of amino acids corresponding to framework sequences allowed positioning 30 of the CDRs (Fig. 5). Taken together, these observed structural features indicate that the amplified and cloned Fv fragments are functional and thus are able to recognize their corresponding antigen, provided they are expressed in appropriate host cells. Accordingly, the 35 murine  $\kappa$  and  $\text{H}$  Fv genes corresponding to the antibody

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produced by the HNK-20 hybridoma have been inserted into expression vectors containing human heavy and light chain constant genes and transfected into myeloma cells.

Materials and Methods

5 Sources of DNA and RNA.

Mouse hybridoma cell line 3G3 (IgM,  $\lambda$ ) was deposited with the American Type Culture Collection, and was assigned ATCC No. HB 8516. Mouse hybridoma cell line HNK-20 (IgA,  $\kappa$ ), from OraVax Inc., Cambridge, USA, was 10 deposited with the American Type Culture Collection (ATCC, Rockville, Maryland) under the provisions of the Budapest Treaty on July 1, 1993, and was assigned ATCC No. HB 11394. Genomic DNA was prepared as described (Gross-Bellard et al., Eur. J. Biochem. 36:32-38, 1973, 15 hereby incorporated by reference). Total RNA was prepared from frozen cell pellets according to the guanidine/cesium chloride method (Glisin et al., Biochemistry 13:2633-2637, 1974; Chirgwin et al., Biochemistry 18:5294-5299, 1979).

20 Synthesis of oligonucleotide primers and probes.

Oligonucleotides were synthesized using standard methods involving the  $\beta$ -cyanoethyl phosphoramidite method and reverse phase HPLC purification (MWG-Biotech, Ebersberg, Germany).

25 DNA amplification by PCR.

In vitro DNA amplification (PCR) was performed in a final volume of 100  $\mu$ l volume using the thermal cycler 9600 from Perkin Elmer (Norwalk, CT). Reagents were added to the reaction to yield the following final 30 composition: 10 mM Tris-HCl pH 8.3 (at 25°C), 50 mM KCl, 2.5 mM MgCl<sub>2</sub>, 0.001% gelatin (Sigma, Cat. No. G2500, St. Louis, MO), 200  $\mu$ M dNTPs, 150 nM of each amplification primer, 1  $\mu$ g of genomic DNA, and 2.5 units of AmpliTaq DNA polymerase (Perkin Elmer, Norwalk, CT). The cycling 35 profile used is as follows: 5 minutes at 94°C; 3 cycles

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of 1 minute at 94°C, 1 minute at 50°C, and 1 minute at 72°C; 27 cycles of 1 minute at 94°C, 1 minute at 62°C, 1 minute at 72°C; and a final incubation at 72°C for 10 minutes.

5 Northern and Southern blot analysis.

Total RNA (10 µg) was denatured with glyoxal and fractionated by electrophoresis on an agarose gel (McMaster et al., Proc. Natl. Acad. Sci. USA 74:4835-4838, 1977). Transfer of RNA onto Gene Screen Plus membrane (Dupont, Wilmington, DE) was carried out according to the procedure described by the manufacturer. PCR products and genomic DNA prepared from hybridoma cells were fractionated on agarose gels and transferred onto Gene Screen Plus membrane as described (Chomczynski et al., Biochem. Biophys. Res. Commun. 122:340-344, 1984).

Northern and Southern blots were hybridized in identical conditions with <sup>32</sup>P-labeled oligonucleotide probes specific for each of the Jλ, Jκ, and JH segments.

20 The temperatures used for prehybridization and hybridization were TM-4°C, while the temperatures used for washing were TM-2°C. The melting temperatures (TMs) of the oligonucleotides were estimated by the formula: TM = 4(G+C) + 2(A+T). The TMs of the J-specific 25 oligonucleotide probes are as follows: Jλ1 = 58°C, Jλ2 = 62°C, Jλ3 = 60°C, Jλ4 = 58°C, Jκ1 = 64°C, Jκ2 = 64°C, Jκ3 = 56°C, Jκ4 = 64°C, Jκ5 = 62°C, JH1 = 68°C, JH2 = 64°C, JH3 = 64°C, and JH4 = 60°C. For both Southern and Northern blots probed with oligonucleotide probes, the 30 following conditions were used. Prehybridization was carried out for 3-4 hours in 2x SSC, 5x Denhardts, 0.1% SDS, and 5 mM EDTA. Hybridization was carried out for 14-18 hours in 5x SSC, 10x Denhardts, 20 mM sodium phosphate buffer (pH 7.0), 7% SDS, 100 µg/ml denatured 35 herring sperm DNA, and <sup>32</sup>P-labeled oligonucleotide (106

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cpm/ml). After hybridization, the membranes were washed twice for 30 minutes in 3x SSC, 10x Denhardts, 5% SDS, and 70 mM sodium phosphate buffer (pH 7.0); and twice for 30 minutes in 1x SSC and 1% SDS.

5 As an internal control for total RNA loading, Northern blots were hybridized with a glyceraldehyde-3-phosphate-dehydrogenase cDNA probe (Piechaczyk et al., Nucleic Acids Res. 12:6951-6963, 1984). For both Northern and Southern blots probed with the cDNA probe,  
10 the following conditions were used. Prehybridization was carried out for 3-5 hours at 42°C in 50% deionized formamide, 5x Denhardts, 5x SSPE (30x SSPE = 4.5 M NaCl, 0.3 M NaH<sub>2</sub>PO<sub>4</sub>, 30 mM EDTA, pH 7.7), 1% SDS, and 200 µg/ml denatured salmon sperm DNA. Hybridization was carried  
15 out for 14-18 hours at 42°C in the same buffer including <sup>32</sup>P-labeled cDNA probe (106 cpm/ml). After hybridization, the membranes were washed twice for 5 minutes in 2x SSPE at room temperature, once for 15 minutes in 2x SSPE and 0.5% SDS at 65°C, and once for 15 minutes in 0.5x SSPE at  
20 65°C.

#### DNA sequencing.

DNA sequences were determined by subcloning the L-VH-D-JH and L-VL-JL PCR fragments in the expression vector pING (Liu et al., Gene 54:33-40, 1987), followed  
25 by sequencing using the dideoxy chain termination method (Sanger et al., Proc. Natl. Acad. Sci. USA 74:5463-5467, 1977).

#### Other Embodiments

The invention also includes any biologically active fragment or analog of the genes and antibodies of the invention. By "biologically active" is meant possessing any activity which is characteristic of HNK-20 variable genes or chimeric antibodies containing them. The invention also includes analogs of the HNK-20

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immunoglobulin variable chains. Preferred analogs include those with sequences which differ from the sequences shown in Figs. 5B-5D only by conservative amino acid substitutions, for example, substitution of one 5 amino acid for another with similar characteristics (e.g., valine for glycine, arginine for lysine, etc.) or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not abolish the immunoglobulin's biological activity. Analogs of the 10 invention will generally exhibit at least 70%, preferably 80%, more preferably 90%, and most preferably 95%, or even 99%, homology with a segment of 20 amino acid residues, preferably 40 amino acid residues, or more preferably the entire sequence of an immunoglobulin of 15 the invention. Alterations in the primary sequence include genetic variants, both natural or induced. Also included are analogs that include residues other than naturally occurring or synthetic amino acids, e.g.,  $\beta$  or  $\gamma$  amino acids. Also included are immunoglobulins 20 modified by in vivo chemical derivitization, including acetylation, methylation, phosphorylation, carboxylation, or glycosylation.

In addition to substantially full-length polypeptides, the invention also includes biologically 25 active fragments of the immunoglobulins, which can be made using standard methods in the art. As used herein, the term "fragment," as applied to a polypeptide, such as an immunoglobulin, will ordinarily be at least 20 residues, more preferably at least 40 residues in length. 30 Similarly, the invention also includes fragments of the genes encoding the immunoglobulins of the invention.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof 35 will be suggested to persons skilled in the art and are

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**to be included within the spirit and scope of this  
application and the appended claims.**

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SEQUENCE LISTING

**(1) GENERAL INFORMATION:**

- (i) APPLICANT: Berdoz, Jose  
Kraehenbuhl, Jean Pierre
- (ii) TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC VARIABLE REGIONS OF IMMUNOGLOBULIN GENES

- (iii) NUMBER OF SEQUENCES: 108

- (iv) CORRESPONDENCE ADDRESS:
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  - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/348,548
  - (B) FILING DATE: 01-DEC-1994

- (viii) ATTORNEY/AGENT INFORMATION:
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**(2) INFORMATION FOR SEQ ID NO:1:**

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 537 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCGTCGAC CGTGGTTGT GAATTATGGC CTGGATTCA CTTATACTCT CTCTCCTGGC	60
TCTCAGCTCA GGTCAGCAGC CTTTCTACAC TGCAGTGGGT ATGCAACAAT GCGCATCTTG	120
TCTCTGATTT GCTACTGATG ACTGGATTTC TCATCTGTTT GCAGGGGCCA TTTCCCAGGC	180
TGTTGTGACT CAGGAATCTG CACTCACCA ACACCTGGT GAAACAGTCA CACTCACTTG	240
TCGCTCAAGT ACTGGGGCTG TTACAACTAG TAACATATGCC AACTGGGTCC AAGAAAAACC	300

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AGATCATTAA	TTCACTGGTC	TAATAGGTGG	TACCAACAAC	CGAGCTCCAG	GTGTTCCCTGC	360
CAGATTCTCA	GGCTCCCTGA	TTGGAGACAA	GGCTGCCCTC	ACCATCACAG	GGGCACAGAC	420
TGAGGATGAG	GCAACATATT	TCTGTGCTCT	ATGGTACAGC	AACCATTGGG	TGTTCGGTGG	480
AGGAACCAAA	CTGACTGTCC	TAGGTGAGTC	ACTGGTCCCT	CCTTTGCCGC	CGCTGAT	537

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Trp	Ile	Ser	Leu	Ile	Leu	Ser	Leu	Leu	Ala	Leu	Ser	Ser	Gly
1					5				10						15
Ala	Ile	Ser	Gln	Ala	Val	Val	Thr	Gln	Glu	Ser	Ala	Leu	Thr	Thr	Ser
					20			25						30	
Pro	Gly	Glu	Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser	Ser	Thr	Gly	Ala	Val
					35			40					45		
Thr	Thr	Ser	Asn	Tyr	Ala	Asn	Trp	Val	Gln	Glu	Lys	Pro	Asp	His	Leu
					50			55			60				
Phe	Thr	Gly	Leu	Ile	Gly	Gly	Thr	Asn	Asn	Arg	Ala	Pro	Gly	Val	Pro
					65			70		75			80		
Ala	Arg	Phe	Ser	Gly	Ser	Leu	Ile	Gly	Asp	Lys	Ala	Ala	Leu	Thr	Ile
					85			90					95		
Thr	Gly	Ala	Gln	Thr	Glu	Asp	Glu	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Trp
					100			105					110		
Tyr	Ser	Asn	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu
					115			120					125		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCGTCGAC	GGACTCAGCA	TGGACATGAG	GACCCCTGCT	CAGTTTCTTG	GAATCTTGT	60
GCTCTGGTTT	CCAGGTAAAA	TGAACAAAAA	TGGGAATGTC	ACTGTGATTA	GTGTTGATTG	120
GCATTTGGGA	GATTTATCT	TTTATGATGC	TTACCTATGT	AGATACTCAT	TATGTCTCCA	180

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TTCCTAGGTA TCAAATGTGA CATCAAGGTG ACCCAGTCTC CATCTTCCAT GTATGCATCT	240
CTAGGAGAGA GAGTCACTAT CACTTGCAAG GCGAGTCAGG ACATTAATAA CTATTAAAC	300
TGGTTCCAGC AGAAACCAGG GAAATCTCCT AAGACCTGAA TCTATCGTGC AAACAGATTG	360
CTAGATGGGG TCCCCTCAAG GTTCAGTGGC AGTGGATCTG GGCAAGATTA TTCTCTCACCC	420
ATCAGCAGCC TGGAGTATGA AGATATGGGA ATTTATTATT GTCTACAGTT TGACCGAGTTT	480
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAC GTAAGTAGTC TTCTCAACTC	540
TTGGGGCCGC TGAT	554

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Thr Pro Ala Gln Phe Leu Gly Ile Leu Leu Leu Trp Phe Pro  
1 5 10 15

Gly Ile Lys Cys Asp Ile Lys Val Thr Gln Ser Pro Ser Ser Met Tyr  
 20 25 30

Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp  
35 40 45

Ile Asn Asn Tyr Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro  
50 55 60

Lys Thr Leu Ile Tyr Arg Ala Asn Arg Leu Leu Asp Gly Val Pro Ser  
55 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser  
85 90 95

Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Phe Asp  
100 105 110

Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTCCGCTGAG TTCCGAGCTCT CAGAGATGGA GACAGACACA CTCCTGTTAT GGGTACTGCT

60

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GCTCTGGGTT CCAGGTGAGA GTGCAGAGAA GTGTTGGATG CAACCTCTGT GGCCATTATG	120
ATACTCCATG CCTCTCTGTT CTTGATCACT ATAATTAGGG CATTGTCAC TGGTTTAAG	180
TTTCCCCAGT CCCCTGAATT TTCCATTCC TCAGAGTGAT GTCCAAAATT CTTCTTAAAA	240
ATTTAAATCA AAAGGTCTC TGCTGTGAAG TCTTTATAC ATATATAACA ATAATCTTG	300
TGTTTATCAT TCCAGGTCC ACTGGTGACA TTGTGCTGAC ACAGTCTCCT GCTTCCTTAG	360
CTGTATCTCT GGGGCAGAGG GCCACCCTCT CATAACGGGC CAGCAAAGT GTCAGTACAT	420
CTGGCTATAG TTATATGGCG TGGAACCAAC AGAAACCCAGG ACAGCCACCC AGACTCCTCA	480
TCTATCTTGT ATCCAACCTA GAATCTGGGG TCCCTGCCAG GTTCAGTGGC AGTGGGTCTG	540
GGACAGACTT CACCCCTCAAC ATCCATCCTG TGGAGGAGGA GGATGCTGCA ACCTATTACT	600
GTCAGCACAT TAGGGAGCTT ACACGTTCGG AGGGGGGACC AAGCTGGAAA TAAAACGTAA	660
GTAGTCTTCT CAACTCTTGC GGCGCGTGT	690

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Trp	Val	Pro
1					5				10				15	

Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala
					20			25				30			

Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Tyr	Arg	Ala	Ser	Lys	Ser
					35			40			45				

Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	Ala	Trp	Asn	Gln	Gln	Lys	Pro
					50			55			60				

Gly	Gln	Pro	Pro	Arg	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Asn	Leu	Glu	Ser
					65			70		75		80			

Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
					85			90				95			

Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
					100			105			110			

Gln	His	Ile	Arg	Glu	Leu	Thr	Arg	Ser	Glu	Gly	Gly	Pro	Ser	Trp	Lys
					115			120			125				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs

- 32 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCGTCGAC CTCAAGGTCC TTACAATGAA ATGCAGCTGG GTCATCTTCT TCCTGATGGC	60
AGTGGTTACA GGTAAGGAGC TCCCAAGTCC CAAACTTGAG GGGCCATACA CTCTGTGACA	120
GTGGCAGTCA CTTTGCCTTT CTTTCTACAG GGGTCAATTG AGAGGTTTCAG CTGCAGCAGT	180
CTGGGGCTGA GCTTGTGAGG CCAGGGGCCT TAGTCAAGTT GTCCTGAAA GCCTCTGGCT	240
TCAACATTAAGA GACTACTAT ATGTACTGGG TAAAACAGAG GCCTGAACAG GGCCTGGAGT	300
GGATTGGATG GATTGATCCT GAAAATGGTA ATACTGTTA TGACCCGAAG TTCCAGGGCA	360
AGGCCAGTAT AACAGCAGAC ACATCCTCCA ACACAGCCTA CCTGCAGCTC AGCAGCCTGG	420
CATCTGAGGA CACTGCCGTC TATTACTGTG CTTACTACGG TACTAGCTAC TGGTTTCCTT	480
ACTGGGGCCA AGGGACTCTG GTCACTGTCT CTGCAGGTGA GTCCTACCTT CTCCGGGCC	540
<b>GCTGAT</b>	<b>546</b>

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 136 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Val	
1 5 10 15	
Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro	
20 25 30	
Gly Ala Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys	
35 40 45	
Asp Tyr Tyr Met Tyr Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu	
50 55 60	
Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Val Tyr Asp Pro	
65 70 75 80	
Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn Thr	
85 90 95	
Ala Tyr Leu Gln Leu Ser Ser Leu Ala Ser Glu Asp Thr Ala Val Tyr	
100 105 110	
Tyr Cys Ala Tyr Tyr Gly Thr Ser Tyr Trp Phe Pro Tyr Trp Gly Gln	
115 120 125	

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Gly Thr Leu Val Thr Val Ser Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCGTCGAC CTTGGTTTGT GAATTATG

28

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCGTCGAC AGTAGTACCT GCATTATG

28

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCGCGGCC GCAAAGGAGG AGGAGTTAC

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCAGCGGCC GCAAGAACCA TAAAGCCAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCAGCGGCC GCAAGAAGCT TTGAAACTAC

30

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATCGTCGAC AAATTCAAAK ACAMAAT

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCGTCGAC AAGACTCAGC CTGACATG

28

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGTCGAC AAGTTCAAAAG ACAAAATG

28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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GATCGTCGAC AGACTCAGCC TGACATG

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATCGTCGAC AGCAGGGGGA GCAGGATG

28

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATCGTCGAC AGGGAAAGTT TGAAGATG

28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATCGTCGAC ATACATCAGA CCAGCATG

28

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATCGTCGAC ATCTAGYTCT CAGAGATG

28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCGTCGAC ATGCATCACA CCAGGCATG

28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCGTCGAC CACCAAGTTC TCAGAAATG

28

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCGTCGAC CAGAGCAGCA GGGACATG

28

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCGTCGAC CAGGGACAAAG TGGGAATG

28

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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GATCGTCGAC CATTCAAGAAC TCAGCATG

28

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATCGTCGAC GCGAGTCAGA CCAGCATG

28

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATCGTCGAC GGACACAGTT TAGATATG

28

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTCGAC GGACTCAGCA TGGACATG

28

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGTCGAC GGAGACGTTG TAGAAATG

28

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCGTCGAC GGATAACACCA TCAGCATG

28

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GATCGTCGAC GGCAARGGCA TCAAGATG

28

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GATCGTCGAC GGCAGKGGRA GCAAGAT

27

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGTCGAC GGTACACAGCA CAAACATG

28

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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GATCGTCGAC GGTTGCCTCC TCAAAATG

28

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GATCGTCGAC GTTCATTTC C TCAAAATG

28

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCGTCGAC TATCAAGTTC TCAGAATG

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCGTCGAC TCTCAAGTTC TCAGAATG

28

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGTCGAC TCTTGTGAAT TAATCATG

28

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GATCGTCGAC TGAAAACACA CAGACATG

28

(2) INFORMATION FOR SEQ ID NO:41:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCGTCGAC TGATAAAAGCC AAGGAATG

28

(2) INFORMATION FOR SEQ ID NO:42:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGTCGAC TGATCACACA CAGWCATG

28

(2) INFORMATION FOR SEQ ID NO:43:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATCGTCGAC TTCCAGCTCT CAGAGATG

28

(2) INFORMATION FOR SEQ ID NO:44:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

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ATCAGCGGCC GCAGAGASTT TGGATTCTAC

30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATCAGCGGCC GCAAGAGTTG AGAAGACTAC

30

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCAGCGGCC GCAGTTGAGC AAAATGTAC

30

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATCAGCGGCC GCAAATGAGC AAAARTCTAC

30

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAGCGGCC GCAAGATGAG AAAAGTGTAC

30

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATCGTCGAC ACACAGACTC ACACCATG

28

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCGTCGAC ACACAGGACC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCGTCGAC ACACAGGATC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCGTCGAC ACACAGGGCA TTGCCATG

28

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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GATCGTCGAC ACACTGACTC AAAACATG

28

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCGTCGAC ACACTGACTC AAACCATG

28

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCGTCGAC ACACTGACTC ACACCATG

28

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GATCGTCGAC ACACTGACTC CAACCATG

28

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCGTCGAC ACACTGACTC TAACCATG

28

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCGTCGAC ACACTGACTC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATCGTCGAC ACACTGACTT CACCATG

27

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GATCGTCGAC ACATAGACTC TAACCATG

28

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCGTCGAC ACATTGACTC AAACCATG

28

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

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GATCGTCGAC AGCCTCCATC AGAGCATG

28

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GATCGTCGAC AGCCTCCGTC AGAGCATG

28

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GATCGTCGAC ATTATAACAT TGAACATG

28

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATCGTCGAC CAAGTCTTAG ACATCATG

28

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GATCGTCGAC CACACATCCC TTACCATG

28

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCGTCGAC CACAGACACC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATCGTCGAC CACAGACCMC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GATCGTCGAC CACAGACCTG TCAACATG

28

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATCGTCGAC CACAGACCTG TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

- 47 -

GATCGTCGAC CACGGAACCC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCGTCGAC CACGGACCCCC TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GATCGTCGAC CACGGACCCCC TCACGATG

28

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GATCGTCGAC CACTCGACTC TAACCATG

28

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GATCGTCGAC CACTGGTGTG CAGTCATG

28

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

- 48 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GATCGTCGAC CACTTCTTAG ACATCATG

28

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATCGTCGAC CAGAGTCCAC TCRCCATG

28

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GATCGTCGAC CCTGTCACTG ACTTCATG

28

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GATCGTCGAC CTCAAGGTCC TTACAATG

28

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

- 49 -

GATCGTCGAC CTCCAGGTCC TTACAATG

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATCGTCGAC CTCAGTCCTG TCACCATG

28

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GATCGTCGAC CTCAGTCCTG TCACTATG

28

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GATCGTCGAC GCAGAGGACC TCACAATG

28

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GATCGTCGAC GCCTTTACAG ACTTCATG

28

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid

- 50 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GATCGTCGAC GGACCTCACCA ATGGGATG

28

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GATCGTCGAC GGGTGTTGCC TAAGGATG

28

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATCGTCGAC GGTGTWGCCT AAAAGATG

28

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GATCGTCGAC GGTGTTGCCT AAAGGATG

28

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

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GATCGTCGAC GTTGTAGCCT AAAAGATG

28

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATCGTCGAC TCAGTCCTTG TCACTATG

28

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATCAGCGGCC GCAAAGAAAA AAGCCAGCTT AC

32

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATCAGCGGCC GCGAGGTTKT AAGGACTCAC

30

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATCAGCGGCC GCGGAGAART TAGGACTCAC

30

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATCAGCGGCC GCGGAGAAGK TAGGACTCAC

30

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATCAGCGGCC GCTGGAGAGG CCATTCTTAC

30

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTCAGTTGG TTCCTCCAC

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTGACCTTGG TTCCACCGC

19

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

- 53 -

GTGACCTTGG TTCCACTGC

19

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTCAATCTGG TTCCACCTC

19

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGCCTCCAC CGAACGTCC

19

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTCCCCCCTC CGAACGTGT

19

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTCCCCATCAC TGAATGTGA

19

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid

- 54 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTCCCCGAGC CGAACGTGA

19

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTCCCAGCAC CGAACGTGA

19

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GACCGTGGTC CCTGCGCCC

19

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGAGTGGTG CCTTGGCCC

19

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

- 55 -

GACCAAGAGTC CCTTGGCCC

19

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACTGAGGTT CCTTGACCC

19

What is claimed is:

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1. Substantially pure DNA encoding a variable region of the antibody produced by hybridoma cell line HNK-20.

2. The DNA of claim 1, wherein said variable  
5 region is from the immunoglobulin heavy chain of said antibody.

3. The DNA of claim 1, wherein said variable region is from the immunoglobulin light chain of said antibody.

10 4. The DNA of claim 1, further encoding an immunoglobulin constant region.

5. The DNA of claim 4, wherein said immunoglobulin constant region is a human immunoglobulin constant region.

15 6. The DNA of claim 4, wherein said DNA encodes an immunoglobulin  $\alpha$  heavy chain.

7. The DNA of claim 1, wherein said DNA is genomic DNA.

8. The DNA of claim 1, wherein said DNA is cDNA.

20 9. Substantially pure DNA comprising the sequence of Fig. 5B, or degenerate variants thereof, and encoding the amino acid sequence of Fig. 5B.

10. Substantially pure DNA comprising a sequence having about 50% or greater sequence identity to the DNA  
25 sequence of Fig. 5B.

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11. Substantially pure DNA which a) is capable of hybridizing to the DNA sequence of Fig. 5B under stringent conditions; and b) encodes a polypeptide having a biological activity of a HNK-20 variable region.

5 12. Substantially pure DNA comprising the sequence of Fig. 5C, or degenerate variants thereof, and encoding the amino acid sequence of Fig. 5C.

13. Substantially pure DNA comprising a sequence having about 50% or greater sequence identity to the DNA  
10 sequence of Fig. 5C.

14. Substantially pure DNA which a) is capable of hybridizing to the DNA sequence of Fig. 5C under stringent conditions; and b) encodes a polypeptide having a biological activity of a HNK-20 variable region.

15 15. Substantially pure DNA comprising the sequence of Fig. 5D, or degenerate variants thereof, and encoding the amino acid sequence of Fig. 5D.

16. Substantially pure DNA comprising a sequence having about 50% or greater sequence identity to the DNA  
20 sequence of Fig. 5D.

17. Substantially pure DNA which a) is capable of hybridizing to the DNA sequence of Fig. 5D under stringent conditions; and b) encodes a polypeptide having a biological activity of a HNK-20 variable region.

25 18. The DNA of claim 1, wherein said DNA is operably linked to regulatory sequences for expression of said variable region; and

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wherein said regulatory sequences comprise a promoter.

19. A vector comprising the DNA of claim 1.

20. A cell comprising the DNA of claim 1.

5 21. A recombinant antibody comprising a variable region from the monoclonal antibody produced by hybridoma cell line HNK-20.

10 22. The recombinant antibody of claim 21, wherein said variable region is from the immunoglobulin heavy chain of said monoclonal antibody.

23. The recombinant antibody of claim 21, wherein said variable region is from the immunoglobulin light chain of said monoclonal antibody.

15 24. The recombinant antibody of claim 21, further comprising a human immunoglobulin constant region.

25. The recombinant antibody of claim 21, further comprising an immunoglobulin  $\alpha$  heavy chain.

20 26. A method of making a recombinant antibody comprising a variable region from the monoclonal antibody produced by hybridoma cell line HNK-20, said method comprising the steps of:

a. providing DNA encoding said variable region of said monoclonal antibody, said DNA further encoding a constant region;

25 b. expressing said DNA.

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27. A method of making a recombinant antibody comprising a variable region from the monoclonal antibody produced by hybridoma cell line HNK-20, said method comprising the steps of:

- 5        a. providing a cell containing DNA encoding said variable region of said monoclonal antibody, said DNA further encoding a constant region;
- b. culturing said cell under conditions in which said recombinant antibody is produced; and
- 10      c. purifying said recombinant antibody from said cell or from the supernatant in which said cell was cultured.

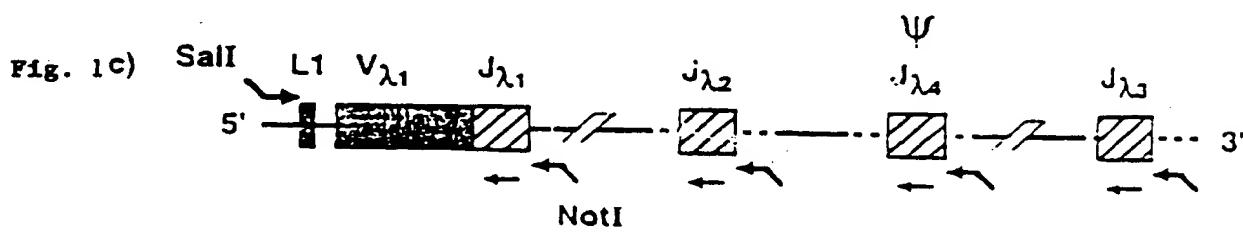
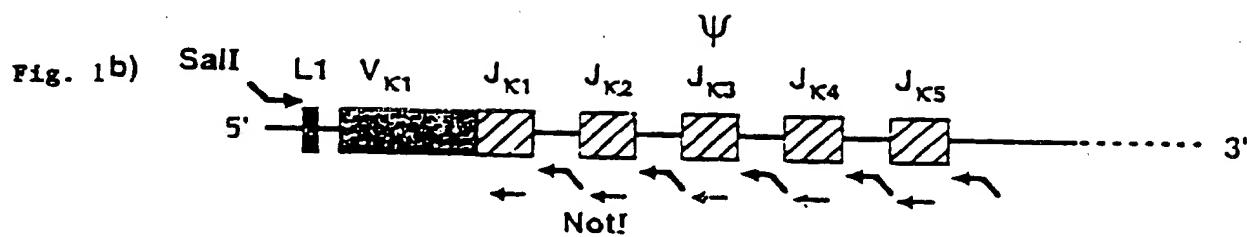
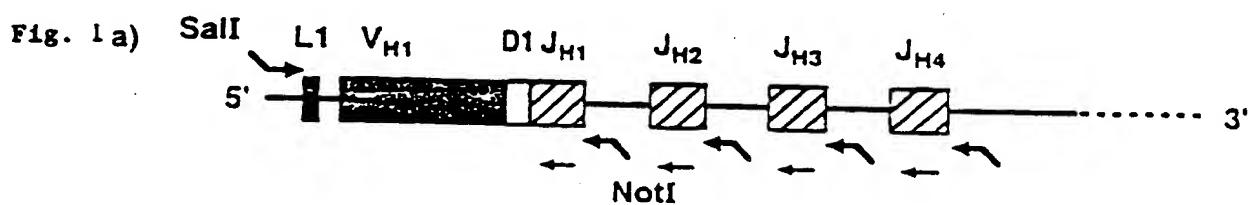
28. A method of isolating a nucleic acid comprising a variable region of an immunoglobulin gene, 15 said method comprising the steps of:

- a. providing genomic DNA comprising said immunoglobulin gene;
- b. providing a first set of primers, each of which contains the sequence of a polymorphic variant of a 20 segment of the 5' untranslated region of said immunoglobulin gene;
- c. providing a second set of primers, each of which contains the sequence of a polymorphic variant of a segment of the intron 3' to the rearranged J region of 25 said immunoglobulin gene;
- d. carrying out a polymerase chain reaction with said genomic DNA and said first and said second sets of primers;
- e. identifying a set of primers from said 30 polymerase chain reaction that comprise sequences of said immunoglobulin gene; and
- f. amplifying said immunoglobulin gene with said identified set of primers.

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29. The method of claim 28, wherein said immunoglobulin gene is from hybridoma cell line HNK-20.

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FIG. 2A

 $J_{\lambda_1}$ ,  $J_{\lambda_2}$ ,  $J_{\lambda_3}$ ,      GAPDH

28S →

18S → —



FIG. 2B

 $J_{K_1}$ ,  $J_{K_2}$ ,  $J_{K_3}$ ,  $J_{K_4}$ ,  $J_{K_5}$ ,      GAPDH

28S →

18S → —

 $J_{H_1}$ ,  $J_{H_2}$ ,  $J_{H_3}$ ,  $J_{H_4}$ ,      GAPDH

28S →

18S → —



FIG. 3A

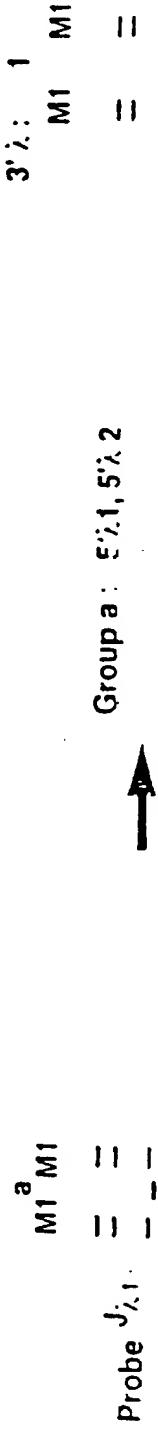
Group of 5'  $\lambda$  primers

FIG. 3B

Groups of 5'  $\kappa$  primers

FIG. 3C

## Groups of 5' H primers

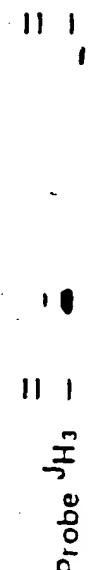


FIG. 3F

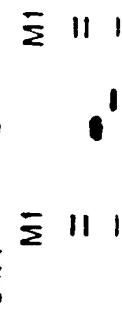
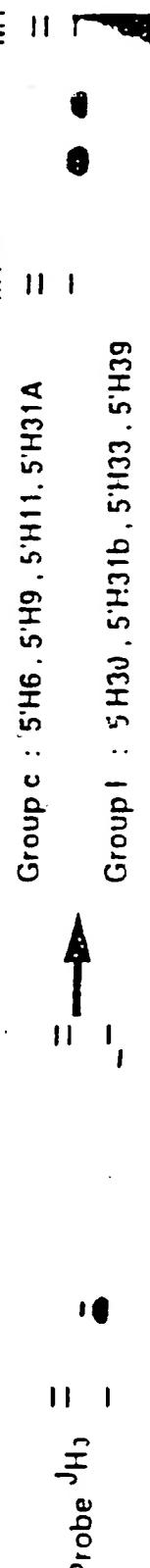
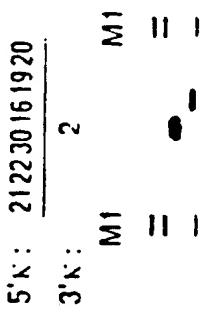
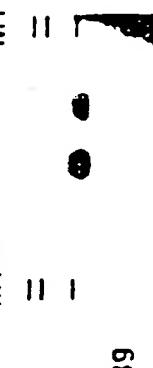
5'K :  $\frac{212230161920}{2}$ Group i :  $5'\kappa 16, 5'\kappa 19, 5'\kappa 20$ Probe  $J_{\kappa_2}$ 

FIG. 3G

5'H :  $\frac{691113130313339}{AB}$ Probe  $J_{H_3}$ 5'K :  $\frac{212230161920}{2}$ Group g :  $5'\kappa 21, 5'\kappa 22, 5'\kappa 30$ Probe  $J_{\kappa_2}$ 5'H :  $\frac{691113130313339}{AB}$ Probe  $J_{H_3}$

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Fig. 4a

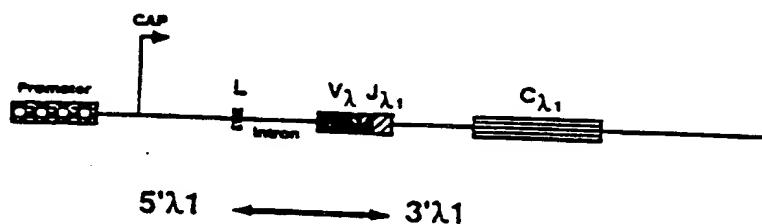


Fig. 4b

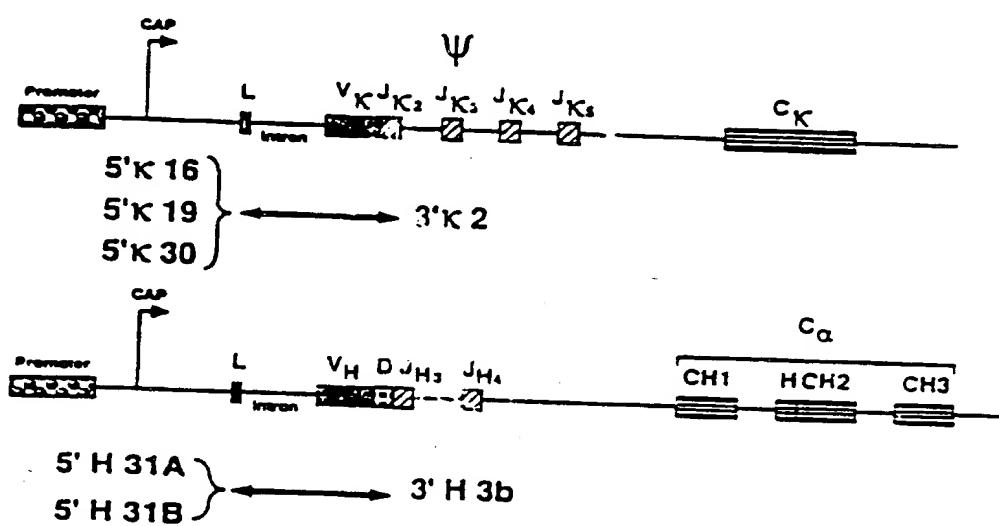


FIG. 4B

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FIG. 5A

GATCOTGACCGTGTGGTAAATGCCC TCC ATT TCA CTT ATA CTC TCT CTC 55  
 Met Ala Thr Ile Ser Leu Ile Leu Ser Leu 10                    SEQ ID NO: 1  
 SEQ ID NO: 2

CTG CCT CTC AGC TCA C CTC ACC AGC CTT TCA CACTGCCACTGGTATCCAACAATGCCAT 116  
 Leu Ala Leu Ser Ser C 15

CCTGCTCTCATTTCTACTCATCTGCATTCTCATCTCTTCCAG CG CCC ATT TCC CAG 178  
 by Ala Ile Ser Cln 20

CCT GTT CTC ACT CAG CAA TCT GCA CTC ACC ACA TCA CCT CCT GAA ACA CTC 229  
 Ala Val Val Thr Cln Glu Ser Ala Leu Thr Ser Pro Gly Glu Thr Val 17

ACA CTC ACT TCT CCC TCA ACT ACT CCC CCT GTT ACA ACT ACT AAC TAT CCC 280  
Thr Leu Thr Cys Arg Ser Ser Thr Cys Ala Val Thr Thr Ser Lys Tyr Ala 54

AAC TCG CTC CAA GAA AAA CCA CAT CAT TTA TTC ACT CCT CTA ATA CCT CCT 331  
Aib Thr Val Cln Glu Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly Glx 71

ACC AAC AAC CGA CCT CCT CCT CCC AGA TTC TCA CCC TCC CTC ATT 382  
Thr Asn Asn Asp Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile 88

CGA GAC AAG CCT CCC CTC ACC ATC ACA CGG CCA CAG ACT GAG GAT GAG GCA 433  
 Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Cln Thr Glu Asp Glu Ala 105

ATA TAT TTC TGT CCT CTA TGG TAC ACC AAC CAT TGG CTC TTC CCT GGA GGA 484  
Ile Tyr Phe Cys Ala Leu Thr Tyr Ser Lys His Thr Val Phe Gly Gly Gly 122

ACC AAA CTC ACT CTC CTA C CTC ACT CTC ACT CTC CCT CCT CCT CCT CCT CCT 537  
Thr Lys Leu Thr Val Leu 128

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## FIG. 5B

B

GATCOTCAACGACTCAACATGACATG	ACG ACC CCT CCT CAG TTT CTT GGA ATC	55	SEQ ID NO: 3
	Met Arg Thr Pro Ala Gln Phe Leu Gly Ile	10	SEQ ID NO: 4
TTC TTG CTC TCG TTT CCA G CTAAAATCAACTAAAATCCAAATCTCACCTGTATTAGTCTTC	116		
Leu Leu Leu Trp Phe Pro G	16		
ATTCGCCATTTCGGAGATTATCTTTATGATCCTAACCTATGTAGATACTCATTATCTCCATTG	193		
CTAC CT ATC AAA TCT GAC ATC AAC GTC ACC CAG TCT CCA TCT TCC ATC TAT	234		
Ile Lys Cys Asp Ile Lys Val Thr Gln Ser Pro Ser Ser Met Tyr	32		
CCA TTT CTA GCA GAG AGA GTC ACT ATC ACT TCC AAC CGG ACT CAG GAC ATT	285		
Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys <u>Lys Ile Ser Gln Asp Ile</u>	49		
AAT AAC TAT TTA AAC TCC TTT GAC CGC AAA CCA CCT AAA TCT CCT AAC ACC	336		
<u>Asn Asn Tyr Ile Ser Thr Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr</u>	66		
CTC ATC TAT CCT CCA AAC AGA TTC CTA CAT CGG GTC CCA TCA AGG TTC ACT	387		
Leu Ile Tyr <u>Arg Ala Ser Asp Leu Ile Asp</u> Gly Val Pro Ser Arg Phe Ser	83		
CCC ACT CCA TCT CGG CAA CAT TAT TCT GTC ACC ATC ACC ACC CTC CAC TAT	438		
Gly Ser Gly Ser Gly Cln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr	100		
GAA GAT ATC GCA ATT TAT TAT TCT CTA CAG TTT GAC GAG TTT CGG TAC ACC	489		
<u>Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Ser Asp Glu Phe Pro Tyr Thr</u>	117		
<u>TTT GGA GGG GGG ACC AAG CTC GAA ATA AAA C GTC AGT GAG TCT TCT CAC TCT TCG</u>	545		
Phe Gln Gly Gly Thr Lys Leu Gln Ile Lys	127		
CCCCCTGAT	554		

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## FIG. SC

C

GATCCTGACTTCCAGCTCTAGAGATG	55	SEQ ID NO: 5
GAG ACA GCA CAC ACA CTC CTC TTA TCG GTC	56	
Met Glu Thr Asp Thr Leu Leu Leu Trp Val	57	SEQ ID NO: 6
CTG CTC CTC TCG GTT CCA G GTCAGAGTCAGAGAACTCTTCGATCCAACCTCTGGCC	115	
Leu Leu Leu Trp Val Pro G	116	
TATGATACTCCATGCCCTCTCTCTTCACTATAATTAGGCATTTCACAGGTTTAAAGTT	182	
TCCCCACTCCCCTGAATTTCGATTTCTCACACTGATGTCGAAATTCTTCTTAAATTAAATC	249	
AAAAGCTCTCTCTCAAGTCCTTATACATATAACAATAATCTTGTCTTATCTTCAG	315	
GT TCC ACT CCT GAC ATT GTG CTC ACA CAG TCT CCT GCT TCC TTA GCT GTC	365	
Ile Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val	366	
TCT CTC CGG CAG ACC CCC ATC TCA TAC AGG CCC AGC AAA ACT GTC ACT	416	
Ser Leu Gly Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser	417	
ACA TCT CCC TAT ACT TAT ATG CAC TCG AAC CAA CAG AAA CCA CGA CAC CCC	467	
Thr Ser Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro	468	
CCC ACA CTC CTC ATC TAT CTT GTC TCC AAC CTA GAA TCT CGG GTC CCT CCC	518	
Pro Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala	519	
AAG TTC ACT CCC ACT CGG TCT CGG ACA GAA TTC ACC CTC AAC ATC CAT CCT	569	
Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro	570	
CTG CAG GAG GAT CCT CCA ACC TAT TAC TCT CAG CAC ATT ATG CAG CTT	620	
Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg Glu Leu	621	
<u>ACA CCT TTT GAG CGG GGA CCA AGC TCG AAA TAA AAC GAAAGTAGTCCTCTCACT</u>	675	
Thr Arg Ser Glu Gly Gly Pro Ser Trp Lys ***	676	
CTTGGCGCCCTGAT	690	

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## FIG. SD

D

GATCCTGACCTCAAGGTCTTACAATG AAA TCC AGC TCG GTC ATC TTC TTC CTC	55	SEQ ID NO: 7
Met Lys Cys Ser Tyr Val Ile Phe Phe Leu	10	SEQ ID NO: 8
ATG CCA GTC GTT ACA G GTAAAGGACCTCCAAAGTCCCAACTTCACGGGCCATACACTCTGT	116	
Met Ala Val Val Thr C	15	
GACAGTCCCACACTTTGCCCTTTCTACAG CG CTC AAT TCA GAG GTT CAG CTG	173	
Ile Val Asn Ser Glu Val Cln Leu	23	
CAG CAC TCT CCC CCT GAG CTT CTC AGC CCA CGG CCC TTA CTC AAC TTG TCC	224	
Gln Cln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Leu Val Lys Leu Ser	40	
TGC AAA CCC TCT CCC TTC AAC ATT AAA GAC TAC TAT ATG TAC TCG CTA AAA	275	
Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr Val Lys Tyr Val Lys	57	
CAG ACC CCT GAA CAG CGC CTC GAG TCG ATT GCA TCG ATT CAT CCT GAA AAT	326	
Gln Arg Pro Glu Cln Gly Leu Glu Tyr Ile Gly Tyr Ile Asp Ser Glu Asn	74	
GCT AAT ACT CTT TAT GAC CCC AAG TTC CAG CGC AAG CCC AST ATA ACA GCA	377	
Gly Asp Thr Val Tyr Asp Pro Lys Phe Glu Gly Lys Ala Ser Ile Thr Ala	91	
GAC ACA TCC TCC AAC ACA CGC TAC CTC CAG CTC AGC ACC CTC GCA TCT GAG	428	
Asp Thr Ser Ser Asn Thr Ala Tyr Leu Glu Leu Ser Ser Leu Ala Ser Glu	108	
GAC ACT CCC GTC TAT TAC TCT CCT TAC CCG ACT ACC TAC TCG TTT CCT	479	
Asp Thr Ala Val Tyr Tyr Cys Ala Tyr Ser Thr Tyr Phe Pro	125	
TAC TCG CCC GAA CGG AAC CCA GTC ACT GTC TCT CCA C GTCAGTCCACCTTCTC	533	
Tyr Tyr Glu Cln Gly Thr Leu Val Thr Val Ser Ala	137	
cccccccccgtar	546	

## FIG. 6A

A) PCR primers for V<sub>λ</sub>:

(a) S<sub>λ</sub>1 : GATCGTCGACCCITGGTTGTGAATTATG  
 (b) S<sub>λ</sub>2 : GATCGTCGACACTAGTACCTGCATTATG  
 3<sub>λ</sub>1 : GATCCCCGGCCCCAAAGGAGGIAGGAGSTIAC  
 3<sub>λ</sub>2 : ATCAGGGGGCCCAGAACCTAAAGCCAC  
 3<sub>λ</sub>3 : ATCAGGGGGCCCAGAACCTTGUAAAATC

SEQ ID NO: 9  
 SEQ ID NO: 10  
 SEQ ID NO: 11  
 SEQ ID NO: 12  
 SEQ ID NO: 13

## FIG. 6B

B) PCR primers for V<sub>κ</sub>:

(a) S<sub>κ</sub>1 : GATCGTCGACAAATTCAAAAGTACAAATC  
 (b) S<sub>κ</sub>2 : GATCGTCGACAAGACTCAGCCTGACATG  
 (c) S<sub>κ</sub>3 : GATCGTCGACAAUTTCAAAAGACAAAAATG  
 (d) S<sub>κ</sub>4 : GATCGTCGACAGACTCAGCCTTIGACATG  
 (e) S<sub>κ</sub>5 : GATCGTCGACAGCAGGGGGAGCAGGATG  
 (f) S<sub>κ</sub>6 : GATCGTCGACAGGGAAAGTTTGUAGATG  
 (g) S<sub>κ</sub>7 : GATCGTCGACATACATGAGAACCCAGCATG  
 (h) S<sub>κ</sub>8 : GATCGTCGACATCTAGCTTCTCAGAGATG  
 (i) S<sub>κ</sub>9 : GATCGTCGACATGCATCACACCACCATG  
 (j) S<sub>κ</sub>10 : GATCGTCGACCAAGTTCTCAGAATG  
 (k) S<sub>κ</sub>11 : GATCGTCGACCAAGCAGCAGCAGGGACATG  
 (l) S<sub>κ</sub>12 : GATCGTCGACCAAGGACAAGTUGGAATG  
 (m) S<sub>κ</sub>13 : GATCGTCGACCCATTCAAGAACTCAGCATG  
 (n) S<sub>κ</sub>14 : GATCGTCGACGGAGTCAGACCAGCATG  
 (o) S<sub>κ</sub>15 : GATCGTCGACGGACACAGTTAGATATG  
 (p) S<sub>κ</sub>16 : GATCGTCGACGGACTCAGCATGGACATG  
 (q) S<sub>κ</sub>17 : GATCGTCGACGGAGACGTTGTAGAAATG  
 (r) S<sub>κ</sub>18 : GATCGTCGACGGATACACCATCAGCATG  
 (s) S<sub>κ</sub>19 : GATCGTCGACGGCAAAGGGCATCAAGATG  
 (t) S<sub>κ</sub>20 : GATCGTCGACGGCAGGTGGA/GAGCAAGAT  
 (u) S<sub>κ</sub>21 : GATCGTCGACGGTACAGCACAAACATC  
 (v) S<sub>κ</sub>22 : GATCGTCGACGGTTGCCCTCTCAAATG  
 (w) S<sub>κ</sub>23 : GATCGTCGACCCATTCAATTUCCIAAAATG  
 (x) S<sub>κ</sub>24 : GATCGTCGACTATCAAGTTCTCAGAATG  
 (y) S<sub>κ</sub>25 : GATCGTCGACTCTCAAGTTCTCAGAATG  
 (z) S<sub>κ</sub>26 : GATCGTCGACCTCTTGTAATCATG  
 (aa) S<sub>κ</sub>27 : GATCGTCGACTGAAAACACACAGACATG  
 (ab) S<sub>κ</sub>28 : GATCGTCGACTGATAAAAGCCAAGGAATG  
 (ac) S<sub>κ</sub>29 : GATCGTCGACTGATCACACACAGATCATG  
 (ad) S<sub>κ</sub>30 : GATCGTCGACTTCCAGCTCTCAGAGATG  
 3<sub>κ</sub>1 : ATCAGGGGGCCCAGAGAG/CTTGGATTCTAC  
 3<sub>κ</sub>2 : ATCAUCUCUCUCUAAGACTTGUAGAAGACTAC  
 3<sub>κ</sub>3 : ATCAGGGGGCCCAGTTGAGCAAAAATGTAC  
 3<sub>κ</sub>4 : ATCAGGGGGCCCAGAACATGAGCAAAAATGTAC  
 3<sub>κ</sub>5 : ATCAGGGGGCCCAGATGAGCAAAAATGTAC

SEQ ID NO: 14  
 SEQ ID NO: 15  
 SEQ ID NO: 16  
 SEQ ID NO: 17  
 SEQ ID NO: 18  
 SEQ ID NO: 19  
 SEQ ID NO: 20  
 SEQ ID NO: 21  
 SEQ ID NO: 22  
 SEQ ID NO: 23  
 SEQ ID NO: 24  
 SEQ ID NO: 25  
 SEQ ID NO: 26  
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 SEQ ID NO: 34  
 SEQ ID NO: 35  
 SEQ ID NO: 36  
 SEQ ID NO: 37  
 SEQ ID NO: 38  
 SEQ ID NO: 39  
 SEQ ID NO: 40  
 SEQ ID NO: 41  
 SEQ ID NO: 42  
 SEQ ID NO: 43  
 SEQ ID NO: 44  
 SEQ ID NO: 45  
 SEQ ID NO: 46  
 SEQ ID NO: 47  
 SEQ ID NO: 48

## FIG. 6C

## C) PCR primers for VH:

(f) SH1 : GATCGTCGACACACAGACTCACACCAG	SEQ ID NO: 49
(g) SH2 : GATCGTCGACACACAGGACCTCACCATG	SEQ ID NO: 50
(j) SH3 : GATCGTCGACACACAGGATCTCACCATG	SEQ ID NO: 51
(g) SH4 : GATCGTCGACACACAGGGCATGCCATG	SEQ ID NO: 52
(b) SH5 : GATCGTCGACACACTGACTCAAAACATG	SEQ ID NO: 53
(e) SH6 : GATCGTCGACACACTGACTCAAACCATG	SEQ ID NO: 54
(j) SH7 : GATCGTCGACACACTGACTCACACCAG	SEQ ID NO: 55
(j) SH8 : GATCGTCGACACACTGACTCTAACCATG	SEQ ID NO: 56
(e) SH9 : GATCGTCGACACACTGACTCTAACCATG	SEQ ID NO: 57
(k) SH10: GATCGTCGACACACTGACTCTCACCATG	SEQ ID NO: 58
(e) SH11: GATCGTCGACACACTGACTCTAACCATG	SEQ ID NO: 59
(m) SH12: GATCGTCGACACATAGACTCTAACCATG	SEQ ID NO: 60
(b) SH13: GATCGTCGACACATTGACTCAAACCATG	SEQ ID NO: 61
(w) SH14: GATCGTCGACAGCCCTCCATCAGACCAG	SEQ ID NO: 62
(e) SH15: GATCGTCGACAGCCCTCCGTCAAGAGCATG	SEQ ID NO: 63
(s) SH16: GATCGTCGACATTATAACATTGAACATG	SEQ ID NO: 64
(b) SH17: GATCGTCGACCAAGTCTTAGACATCATG	SEQ ID NO: 65
(k) SH18: GATCGTCGACCAACATCCCTTACCATG	SEQ ID NO: 66
(h) SH19: GATCGTCGACCCACAGACACCTCACCATG	SEQ ID NO: 67
(e) SH20: GATCGTCGACCCACAGACACCTCACCATG	SEQ ID NO: 68
(k) SH21: GATCGTCGACCCACAGACCTGTACCATG	SEQ ID NO: 69
(h) SH22: GATCGTCGACCCACAGACCTGTACCATG	SEQ ID NO: 70
(e) SH23: GATCGTCGACCCACGGAACCTCACCATG	SEQ ID NO: 71
(l) SH24: GATCGTCGACCCACGGACCCCTCACCATG	SEQ ID NO: 72
(f) SH25: GATCGTCGACCCACGGACCCCTCACCATG	SEQ ID NO: 73
(k) SH26: GATCGTCGACCCACTCGACTCTAACCATG	SEQ ID NO: 74
(h) SH27: GATCGTCGACCCACTGGTGTGCAGTCATG	SEQ ID NO: 75
(e) SH28: GATCGTCGACCCACTTCTAGACATCATG	SEQ ID NO: 76
(f) SH29: GATCGTCGACCCAGAGTCCACTCA/GCCATG	SEQ ID NO: 77
(l) SH30: GATCGTCGACCCCTGTCACTGACTTCATG	SEQ ID NO: 78
(c) SH31: GATCGTCGACCTCAAGGTCTTACAATG	SEQ ID NO: 79
(m) SH31b: GATCGTCGACCTCCAGGTCTTACAATG	SEQ ID NO: 80
(i) SH32: GATCGTCGACCTCACTCAGTCTGTACCATG	SEQ ID NO: 81
(l) SH33: GATCGTCGACCTCACTCTCTCACTATG	SEQ ID NO: 82
(i) SH34: GATCGTCGACCGAGGAGCTCACATG	SEQ ID NO: 83
(d) SH35: GATCGTCGACGCCCTTACAGACTTGATG	SEQ ID NO: 84
(n) SH36: GATCGTCGACGGACCTCACCATGGATG	SEQ ID NO: 85
(i) SH37: GATCGTCGACGGGTGTGCTTAAGGATG	SEQ ID NO: 86
(d) SH38: GATCGTCGACGGGTGTATGCCCTAAAAGATG	SEQ ID NO: 87
(l) SH39: GATCGTCGACGGGTGTCTTAAAGGATG	SEQ ID NO: 88
(z) SH40: GATCGTCGACGGGTAGCCTAAAAGATG	SEQ ID NO: 89
(d) SH41: GATCGTCGACTCAGTCTGTCACTATG	SEQ ID NO: 90
3'H1 : ATCAGGGGGCCAAAGAAAAAAGCCAGCTTAC	SEQ ID NO: 91
3'H2 : ATCACCCCCCCCCGAGGTT/GTAAGGACTCAC	SEQ ID NO: 92
3'H3a: ATCAGGGGGGGGGAGAAA/GTAAAGGACTCAC	SEQ ID NO: 93
3'H3b: ATCAGGGGGGGGGAGAACT/GTAAAGGACTCAC	SEQ ID NO: 94
3'H4 : ATCAGGGGGGGCTGGAGAGGCCATTCTAC	SEQ ID NO: 95

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**FIG. 6D****D) J<sub>λ</sub> oligo probes :**

J <sub>λ1</sub> : GTCAGTTGGTTCCTCCAC	SEQ ID NO: 96
J <sub>λ2</sub> : GTGACCTTGGTCCACCGC	SEQ ID NO: 97
J <sub>λ3</sub> : GTGACCTTGGTCCACTGC	SEQ ID NO: 98
J <sub>λ4</sub> : GTCAATCTGGTCCACCTC	SEQ ID NO: 99

**FIG. 6E****E) J<sub>κ</sub> oligo probes :**

J <sub>κ1</sub> : GTGCCTCCACCGAACGTCC	SEQ ID NO: 100
J <sub>κ2</sub> : GTCCCCCTCCGAACGTGT	SEQ ID NO: 101
J <sub>κ3</sub> : GTCCCCTCACTGAATGTGA	SEQ ID NO: 102
J <sub>κ4</sub> : GTCCCCGAGCCGAACGTGA	SEQ ID NO: 103
J <sub>κ5</sub> : GTCCCAGCACCGAACGTGA	SEQ ID NO: 104

**FIG. 6F****F) J<sub>H</sub> oligo probes :**

J <sub>H1</sub> : GACCGTGGTCCCTGGCCCC	SEQ ID NO: 105
J <sub>H2</sub> : GAGAGTGGTGCCTTGGCCCC	SEQ ID NO: 106
J <sub>H3</sub> : GACCAGAGTCCCTTGGCCCC	SEQ ID NO: 107
J <sub>H4</sub> : GACTGAGGTTCTTGACCC	SEQ ID NO: 108

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US95/15716

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.  
US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.53; 435/320.2, 240.2, 240.42, 91.2, 70.21; 530/387.3, 388.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, CAS ONLINE, BIOSIS

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Journal of Virology, Volume 63, Number 2, issued February 1994, Garcia-Barreno et al., "Marked Differences in the Antigenic Structure of Human Respiratory Syncytial Virus F and G Glycoproteins", pages 925-932, especially figures 3 and 4 on page 928.	1-29
Y	Proceedings of the National Academy of Sciences USA, Volume 86, issued May 1989, Orlandi et al., "Cloning Immunoglobulin Variable Domains for Expression by the Polymerase Chain Reaction", pages 3833-3837, see entire article.	1-29

Further documents are listed in the continuation of Box C.  See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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*O* document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family
*P* document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

15 MARCH 1996

Date of mailing of the international search report

25 MAR 1996

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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/15716

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Bio/Technology, Volume 9, issued March 1991, Tempest et al., "Reshaping a Human Monoclonal Antibody to Inhibit Human Respiratory Syncytial Virus Infection <i>In Vivo</i> ", pages 266-271, see entire article.	1-29
Y	Journal Hyg. Camb., Volume 68, issued 1970, Scott et al., "Respiratory Syncytial Virus Neutralizing Activity in Nasopharyngeal Secretions", pages 581-588, see entire document.	1-29

Form PCT/ISA/210 (continuation of second sheet)(July 1992)\*

**INTERNATIONAL SEARCH REPORT**

International application No.

PCT/US95/15716

**A. CLASSIFICATION OF SUBJECT MATTER:**  
IPC (6):

C07H 15/12; C12N 15/00, 15/13, 5/10, 1/20; C07K 16/08; C12P 19/34, 21/08

**A. CLASSIFICATION OF SUBJECT MATTER:**  
US CL :

536/23.53; 435/320.2, 240.2, 240.42, 91.2, 70.21; 530/387.3, 388.3